

## SEQUENCE LISTING

<110> McCance, Dennis  
Westbrook, III, Thomas F.

<120> E7 REGULATION OF P21 (CIP1) THROUGH AKT

<130> 21108.0016U2

<140> 10/511,814

<141> Unassigned

<150> PCT/US03/12667

<151> 2003-04-21

<150> 60/374,245

<151> 2002-04-19

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

<400> 1

Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser
1				5					10					15	
His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu
			20					25				30			
Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro
			35				40					45			
Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg
			50			55				60					
Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	Arg
65					70				75					80	
Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	Met
				85					90					95	
Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	Val	Asn
			100					105					110		
Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	Tyr	Arg
			115				120					125			
Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	His	Leu
						135					140				
Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	Leu	Cys
145					150					155				160	
Met	Lys	Ala	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	Leu	Lys	
				165				170					175		
Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	Glu	Leu
			180					185					190		
Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	Ser	Arg
			195				200						205		

Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	Ile	Ala
210						215					220				
Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	His	Met
225				230				235							240
Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	Val	Gln
				245				250						255	
Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe	His	Thr
			260					265					270		

Gln

<210> 2  
 <211> 344  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 Synthetic Construct

<400> 2

Trp	Ser	Gln	Pro	Lys	Thr	Pro	Val	Pro	Ala	Gln	Arg	Glu	Arg	Ala	Pro
1				5					10					15	
Val	Ser	Gly	Thr	Gln	Glu	Lys	Asn	Lys	Ile	Arg	Pro	Arg	Gly	Gln	Arg
			20					25					30		
Asp	Ser	Ser	Tyr	Tyr	Trp	Glu	Ile	Glu	Ala	Ser	Glu	Val	Met	Leu	Ser
		35					40					45			
Thr	Arg	Ile	Gly	Ser	Gly	Ser	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Lys	Trp
	50					55					60				
His	Gly	Asp	Val	Ala	Val	Lys	Ile	Leu	Lys	Val	Val	Asp	Pro	Thr	Pro
65					70					75					80
Glu	Gln	Phe	Gln	Ala	Phe	Arg	Asn	Glu	Val	Ala	Val	Leu	Arg	Lys	Thr
				85					90					95	
Arg	His	Val	Asn	Ile	Leu	Leu	Phe	Met	Gly	Tyr	Met	Thr	Lys	Asp	Asn
			100					105					110		
Leu	Ala	Ile	Val	Thr	Gln	Trp	Cys	Glu	Gly	Ser	Ser	Leu	Tyr	Lys	His
		115					120					125			
Leu	His	Val	Gln	Glu	Thr	Lys	Phe	Gln	Met	Phe	Gln	Leu	Ile	Asp	Ile
	130					135					140				
Ala	Arg	Gln	Thr	Ala	Gln	Gly	Met	Asp	Tyr	Leu	His	Ala	Lys	Asn	Ile
145					150					155					160
Ile	His	Arg	Asp	Met	Lys	Ser	Asn	Asn	Ile	Phe	Leu	His	Glu	Gly	Leu
				165					170					175	
Thr	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala	Thr	Val	Lys	Ser	Arg	Trp
			180					185					190		
Ser	Gly	Ser	Gln	Gln	Val	Glu	Gln	Pro	Thr	Gly	Ser	Val	Leu	Trp	Met
		195					200					205			
Ala	Pro	Glu	Val	Ile	Arg	Met	Gln	Asp	Asn	Asn	Pro	Phe	Ser	Phe	Gln
	210					215					220				
Ser	Asp	Val	Tyr	Ser	Tyr	Gly	Ile	Val	Leu	Tyr	Glu	Leu	Met	Thr	Gly
225					230					235					240
Glu	Leu	Pro	Tyr	Ser	His	Ile	Asn	Asn	Arg	Asp	Gln	Ile	Ile	Phe	Met
				245					250					255	
Val	Gly	Arg	Gly	Tyr	Ala	Ser	Pro	Asp	Leu	Ser	Lys	Leu	Tyr	Lys	Asn
			260					265					270		
Cys	Pro	Lys	Ala	Met	Lys	Arg	Leu	Val	Ala	Asp	Cys	Val	Lys	Lys	Val
		275					280					285			
Lys	Glu	Glu	Arg	Pro	Leu	Phe	Pro	Gln	Ile	Leu	Ser	Ser	Ile	Glu	Leu
	290					295					300				
Leu	Gln	His	Ser	Leu	Pro	Lys	Ile	Asn	Arg	Ser	Ala	Ser	Glu	Pro	Ser
305					310					315					320

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<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct
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<210> 4
<211> 164
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct
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[illegible]

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<220>
<223> Description of Artificial Sequence:/Note =
        Synthetic Construct
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&lt;400&gt; 5

Ala	Thr	Gly	Thr	Cys	Ala	Gly	Ala	Ala	Cys	Cys	Gly	Gly	Cys	Thr	Gly	
1				5					10					15		
Gly	Gly	Gly	Ala	Thr	Gly	Thr	Cys	Cys	Gly	Thr	Cys	Ala	Gly	Ala	Ala	
			20					25					30			
Cys	Cys	Cys	Ala	Thr	Gly	Cys	Gly	Gly	Cys	Ala	Gly	Cys	Ala	Ala	Gly	
		35					40					45				
Gly	Cys	Cys	Thr	Gly	Cys	Cys	Gly	Cys	Cys	Gly	Cys	Cys	Thr	Cys	Thr	
	50					55					60					
Thr	Cys	Gly	Gly	Cys	Cys	Ala	Gly	Thr	Gly	Gly	Ala	Cys	Ala	Gly		
65				70					75						80	
Cys	Gly	Ala	Gly	Cys	Ala	Gly	Cys	Thr	Gly	Ala	Gly	Cys	Cys	Gly	Cys	
				85					90					95		
Gly	Ala	Cys	Thr	Gly	Thr	Gly	Ala	Thr	Gly	Cys	Gly	Cys	Thr	Ala	Ala	
			100					105						110		
Thr	Gly	Gly	Cys	Gly	Gly	Gly	Cys	Thr	Gly	Cys	Ala	Thr	Cys	Cys	Ala	
		115					120					125				
Gly	Gly	Ala	Gly	Gly	Cys	Cys	Gly	Thr	Gly	Ala	Gly	Cys	Gly	Ala		
	130					135					140					
Thr	Gly	Gly	Ala	Ala	Cys	Thr	Thr	Cys	Gly	Ala	Cys	Thr	Thr	Thr	Gly	
145				150					155						160	
Thr	Cys	Ala	Cys	Cys	Gly	Ala	Gly	Ala	Cys	Ala	Cys	Cys	Ala	Cys	Thr	
				165					170					175		
Gly	Gly	Ala	Gly	Gly	Gly	Thr	Gly	Ala	Cys	Thr	Thr	Cys	Gly	Cys	Cys	
			180					185					190			
Thr	Gly	Gly	Gly	Ala	Gly	Cys	Gly	Thr	Gly	Thr	Gly	Cys	Gly	Gly	Gly	
		195					200					205				
Gly	Cys	Cys	Thr	Thr	Gly	Gly	Cys	Cys	Thr	Gly	Cys	Cys	Cys	Ala	Ala	
	210					215					220					
Gly	Cys	Thr	Cys	Thr	Ala	Cys	Cys	Thr	Thr	Cys	Cys	Cys	Ala	Cys	Gly	
225				230						235					240	
Gly	Gly	Gly	Cys	Cys	Cys	Cys	Gly	Gly	Cys	Gly	Ala	Gly	Gly	Cys	Cys	
				245					250					255		
Gly	Gly	Gly	Ala	Thr	Gly	Ala	Gly	Thr	Thr	Gly	Gly	Gly	Ala	Gly	Gly	
			260					265					270			
Ala	Gly	Gly	Cys	Ala	Gly	Gly	Cys	Gly	Gly	Cys	Cys	Thr	Gly	Gly	Cys	
		275					280					285				
Ala	Cys	Cys	Thr	Cys	Ala	Cys	Cys	Thr	Gly	Cys	Thr	Cys	Thr	Gly	Cys	
	290					295					300					
Thr	Gly	Cys	Ala	Gly	Gly	Gly	Gly	Ala	Cys	Ala	Gly	Cys	Ala	Gly	Ala	
305				310					315						320	
Gly	Gly	Ala	Ala	Gly	Ala	Cys	Cys	Ala	Thr	Gly	Thr	Gly	Gly	Ala	Cys	
				325					330					335		
Cys	Thr	Gly	Thr	Cys	Ala	Cys	Thr	Gly	Thr	Cys	Thr	Thr	Gly	Thr	Ala	
			340					345					350			
Cys	Cys	Cys	Thr	Thr	Gly	Thr	Gly	Cys	Cys	Thr	Cys	Gly	Cys	Thr	Cys	
		355					360					365				
Ala	Gly	Gly	Gly	Gly	Ala	Gly	Cys	Ala	Gly	Gly	Cys	Thr	Gly	Ala	Ala	
	370					375					380					
Gly	Gly	Gly	Thr	Cys	Cys	Cys	Cys	Ala	Gly	Gly	Thr	Gly	Gly	Ala	Cys	
385				390					395						400	
Cys	Thr	Gly	Gly	Ala	Gly	Ala	Cys	Thr	Cys	Thr	Cys	Ala	Gly	Gly	Gly	
				405					410					415		
Thr	Cys	Gly	Ala	Ala	Ala	Ala	Cys	Gly	Gly	Cys	Gly	Gly	Cys	Ala	Gly	
			420					425					430			
Ala	Cys	Cys	Ala	Gly	Cys	Ala	Thr	Gly	Ala	Cys	Ala	Gly	Ala	Thr	Thr	
		435					440					445				
Thr	Cys	Thr	Ala	Cys	Cys	Ala	Cys	Thr	Cys	Cys	Ala	Ala	Ala	Cys	Gly	
	450					455						460				

Cys Cys Gly Gly Cys Thr Gly Ala Thr Cys Thr Thr Cys Thr Cys Cys  
 465 470 475 480  
 Ala Ala Gly Ala Gly Gly Ala Ala Gly Cys Cys Cys Thr Ala Ala  
 485 490 495

<210> 6  
 <211> 480  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
 Synthetic Construct

<400> 6  
 Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly  
 1 5 10 15  
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp  
 20 25 30  
 Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg  
 35 40 45  
 Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys  
 50 55 60  
 Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp  
 65 70 75 80  
 Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg  
 85 90 95  
 Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys  
 100 105 110  
 Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn  
 115 120 125  
 Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg  
 130 135 140  
 Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr  
 145 150 155 160  
 Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr  
 165 170 175  
 Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val  
 180 185 190  
 Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro  
 195 200 205  
 Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys  
 210 215 220  
 Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser  
 225 230 235 240  
 Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu  
 245 250 255  
 Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr  
 260 265 270  
 Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile  
 275 280 285  
 Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala  
 290 295 300  
 Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val  
 305 310 315 320  
 Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly  
 325 330 335  
 Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln  
 340 345 350  
 Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe  
 355 360 365

```

Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu
  370                      375                      380
Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys
385                      390                      395                      400
Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val
                      405                      410                      415
Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu
                      420                      425                      430
Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr
                      435                      440                      445
Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu
                      450                      455                      460
Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala
465                      470                      475                      480

```

&lt;210&gt; 7

&lt;211&gt; 1443

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 7

```

atgagcgacg tggctattgt gaaggagggt tggctgcaca aacgagggga gtacatcaag      60
acctggcggc cacgctactt cctcctcaag aatgatggca ccttcattgg ctacaaggag      120
cggccgcagg atgtggacca acgtgaggct cccctcaaca acttctctgt ggcgcagtgc      180
cagctgatga agacggagcg gccccggccc aacaccttca tcatccgctg cctgcagtgg      240
accactgtca tcgaacgcac cttccatgtg gagactcctg aggagcggga ggagtggaca      300
accgccatcc agactgtggc tgacggcctc aagaagcagg aggaggagga gatggacttc      360
cggtcgggct caccagtgga caactcaggg gctgaagaga tggagggtgtc cctggccaag      420
ccaagcacc gcgtgaccat gaacgagttt gactacctga agctgctggg caagggcact      480
ttcggcaagg tgatcctggt gaaggagaag gccacaggcc gctactacgc catgaagatc      540
ctcaagaagg aagtcatcgt ggccaaggac gaggtggccc acacactcac cgagaaccgc      600
gtcctgcaga actccaggca ccccttcctc acagccctga agtactcttt ccagaccac      660
gaccgcctct gctttgtcat ggagtacgcc aacgggggcg agctgttctt ccacctgtcc      720
cgggaaacgtg tgttctccga ggaccgggcc cgcttctatg gcgctgagat tgtgtcagcc      780
ctggactacc tgcaactcga gaagaacgtg gtgtaccggg acctcaagct ggagaacctc      840
atgctggaca aggacgggca cattaagatc acagacttcg ggctgtgcaa ggaggggatc      900
aaggacggtg ccaccatgaa gaccttttgc ggcacacctg agtacctggc ccccgagggtg      960
ctggaggaca atgactacgg ccgtgcagtg gactggtggg ggctgggcgt ggtcatgtac     1020
gagatgatgt gcggtcgctt gcccttctac aaccaggacc atgagaagct ttttgagctc     1080
atcctcatgg aggagatccg cttcccgcgc acgcttggtc ccgaggccaa gtccttgctt     1140
tcagggctgc tcaagaagga cccaagcag aggccttggcg ggggctccga ggacgccaaag     1200
gagatcatgc agcatcgctt ctttgccggt atcgtgtggc agcacgtgta cgagaagaag     1260
ctcagcccac ccttcaagcc ccaggtcacg tcggagactg acaccaggta ttttgatgag     1320
gagttcacgg cccagatgat caccatcaca ccacctgacc aagatgacag catggagtgt     1380
gtggacagcg agcgcaggcc ccacttcccc cagtttctct actcggccag cagcacggcc     1440
tga                                                    1443

```

&lt;210&gt; 8

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 8

```

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
 1           5           10           15
Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser
           20           25           30
Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp
           35           40           45
Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr
           50           55           60
Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu
65           70           75           80
Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln
           85           90           95
Lys Pro

```

&lt;210&gt; 9

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 9

```

atgcatggag atacacctac attgcatgaa tatatgtttag atttgcaacc agagacaact      60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga aatagatggt      120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag      180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa      240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca          294

```

&lt;210&gt; 10

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 10

```

atgcacggag atacacctac attgcatgaa tatatgtttag atttgcaacc agagacaact      60
gatctctact gttatgagca attaaatgac agctcagagg aggaggatga aatagatggt      120
ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag      180
tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa      240
gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca          294

```

&lt;210&gt; 11

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 11

```

Met His Gly Asp Thr Pro Thr Leu His Glu Tyr Met Leu Asp Leu Gln
 1           5           10           15

```

Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn Asp Ser Ser  
                   20                  25                  30  
 Glu Glu Glu Asp Glu Val Asp Gly Pro Ala Gly Gln Ala Glu Pro Asp  
           35                  40                  45  
 Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser Thr  
       50                  55                  60  
 Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu Glu  
 65                  70                  75                  80  
 Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile Cys Ser Gln  
                   85                  90                  95  
 Lys Pro

<210> 12  
 <211> 294  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
       Synthetic Construct

<400> 12  
 atgcatggag atacacctac attgcatgaa tatatgtttag atttgcaacc agagacaact 60  
 gatctctact gttatgagca attaaatgac agctcagagg aggaggatga agtagatggt 120  
 ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag 180  
 tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa 240  
 gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca 294

<210> 13  
 <211> 294  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
       Synthetic Construct

<400> 13  
 atgcacggag atacacctac attgcatgaa tatatgtttag atttgcaacc agagacaact 60  
 gatctctact gttatgagca attaaatgac agctcagagg aggaggatga agtagatggt 120  
 ccagctggac aagcagaacc ggacagagcc cattacaata ttgtaacctt ttgttgcaag 180  
 tgtgactcta cgcttcggtt gtgcgtacaa agcacacacg tagacattcg tactttggaa 240  
 gacctgttaa tgggcacact aggaattgtg tgccccatct gttctcagaa acca 294

<210> 14  
 <211> 648  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
       Synthetic Construct

<400> 14  
 Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly  
   1                  5                  10                  15  
 Leu Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile  
           20                  25                  30  
 Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu  
       35                  40                  45



Thr	Asp	Ser	Ser	Lys	Thr	Ser	Asn	Thr	Ile	Arg	Val	Phe	Leu	Pro	Asn
50						55					60				
Lys	Gln	Arg	Thr	Val	Val	Asn	Val	Arg	Asn	Gly	Met	Ser	Leu	His	Asp
65				70						75					80
Cys	Leu	Met	Lys	Ala	Leu	Lys	Val	Arg	Gly	Leu	Gln	Pro	Glu	Cys	Cys
				85					90					95	
Ala	Val	Phe	Arg	Leu	Leu	Gln	Glu	His	Lys	Gly	Lys	Lys	Ala	Arg	Leu
			100					105					110		
Asp	Trp	Asn	Thr	Asp	Ala	Ala	Ser	Leu	Ile	Gly	Glu	Glu	Leu	Gln	Val
		115					120					125			
Asp	Phe	Leu	Asp	His	Val	Pro	Leu	Thr	Thr	His	Asn	Phe	Ala	Arg	Lys
		130				135					140				
Thr	Phe	Leu	Lys	Leu	Ala	Phe	Cys	Asp	Ile	Cys	Gln	Lys	Phe	Leu	Leu
145				150						155					160
Asn	Gly	Phe	Arg	Cys	Gln	Thr	Cys	Gly	Tyr	Lys	Phe	His	Glu	His	Cys
				165					170					175	
Ser	Thr	Lys	Val	Pro	Thr	Met	Cys	Val	Asp	Trp	Ser	Asn	Ile	Arg	Gln
			180					185					190		
Leu	Leu	Leu	Phe	Pro	Asn	Ser	Thr	Ala	Ser	Asp	Ser	Gly	Val	Pro	Ala
		195					200					205			
Pro	Pro	Ser	Phe	Thr	Met	Arg	Arg	Met	Arg	Glu	Ser	Val	Ser	Arg	Met
		210				215					220				
Pro	Ala	Ser	Ser	Gln	His	Arg	Tyr	Ser	Thr	Pro	His	Ala	Phe	Thr	Phe
225				230						235					240
Asn	Thr	Ser	Ser	Pro	Ser	Ser	Glu	Gly	Ser	Leu	Ser	Gln	Arg	Gln	Arg
				245					250					255	
Ser	Thr	Ser	Thr	Pro	Asn	Val	His	Met	Val	Ser	Thr	Thr	Leu	Pro	Val
			260					265					270		
Asp	Ser	Arg	Met	Ile	Glu	Asp	Ala	Ile	Arg	Ser	His	Ser	Glu	Ser	Ala
		275					280					285			
Ser	Pro	Ser	Ala	Leu	Ser	Ser	Ser	Pro	Asn	Asn	Leu	Ser	Pro	Thr	Gly
		290				295					300				
Trp	Ser	Gln	Pro	Lys	Thr	Pro	Val	Pro	Ala	Gln	Arg	Glu	Arg	Ala	Pro
305				310						315					320
Gly	Ser	Gly	Thr	Gln	Glu	Lys	Asn	Lys	Ile	Arg	Pro	Arg	Gly	Gln	Arg
				325					330					335	
Asp	Ser	Ser	Tyr	Trp	Glu	Ile	Glu	Ala	Ser	Glu	Val	Met	Leu	Ser	
			340				345					350			
Thr	Arg	Ile	Gly	Ser	Gly	Ser	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Lys	Trp
			355				360					365			
His	Gly	Asp	Val	Ala	Val	Lys	Ile	Leu	Lys	Val	Val	Asp	Pro	Thr	Pro
			370			375					380				
Glu	Gln	Leu	Gln	Ala	Phe	Arg	Asn	Glu	Val	Ala	Val	Leu	Arg	Lys	Thr
385				390						395					400
Arg	His	Val	Asn	Ile	Leu	Leu	Phe	Met	Gly	Tyr	Met	Thr	Lys	Asp	Asn
			405						410					415	
Leu	Ala	Ile	Val	Thr	Gln	Trp	Cys	Glu	Gly	Ser	Ser	Leu	Tyr	Lys	His
			420					425					430		
Leu	His	Val	Gln	Glu	Thr	Lys	Phe	Gln	Met	Phe	Gln	Leu	Ile	Asp	Ile
			435				440					445			
Ala	Arg	Gln	Thr	Ala	Gln	Gly	Met	Asp	Tyr	Leu	His	Ala	Lys	Asn	Ile
			450			455					460				
Ile	His	Arg	Asp	Met	Lys	Ser	Asn	Asn	Ile	Phe	Leu	His	Glu	Gly	Leu
465				470						475					480
Thr	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala	Thr	Val	Lys	Ser	Arg	Trp
				485					490					495	
Ser	Gly	Ser	Gln	Gln	Val	Glu	Gln	Pro	Thr	Gly	Ser	Val	Leu	Trp	Met
			500					505					510		
Ala	Pro	Glu	Val	Ile	Arg	Met	Gln	Asp	Asn	Asn	Pro	Phe	Ser	Phe	Gln
			515				520					525			

```

Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly
  530                      535                      540
Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met
545                      550                      555                      560
Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Arg Leu Tyr Lys Asn
                      565                      570                      575
Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val
                      580                      585                      590
Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu
                      595                      600                      605
Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu Pro Ser
                      610                      615                      620
Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr Leu Thr
625                      630                      635                      640
Thr Ser Pro Arg Leu Pro Val Phe
                      645

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&lt;210&gt; 15

&lt;211&gt; 2977

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 15

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ccgaatgtga ccgcctcccc ctccctcacc cgccgcgggg aggaggagcg ggcgagaagc      60
tgccgcgcaa cgacaggacg ttggggcggc ctggctccct caggtttaag aattgtttaa      120
gctgcatcaa tggagcacat acaggagact tggagacga tcagcaatgg ttttggattc      180
aaagatgccg tgtttgatgg ctccagctgc atctctccta caatagttca gcagtttggc      240
tatcagcgcc gggcatcaga tgatggcaaa ctcacagatc cttctaagac aagcaacact      300
atccgtgttt tcttgccgaa caagcaaaga acagtgggtc atgtgcgaaa tggaatgagc      360
ttgcatgact gccttatgaa agcactcaag gtgagggggc tgcaaccaga gtgctgtgca      420
gtgttcagac ttctccacga acacaaaggt aaaaaagcac gcttagattg gaatactgat      480
gctgcgctct tgattggaga agaacttcaa gtagatttcc tggatcatgt tcccctcaca      540
acacacaact ttgctcggaa gacgttcctg aagcttgctt tctgtgacat ctgtcagaaa      600
ttctgtctca atggatttcg atgtcagact tgtggctaca aatttcatga gcactgtagc      660
accaaagtac ctactatgtg tgtggactgg agtaacatca gacaactctt attgtttcca      720
aattccacta ttggtgatag tggagtccca gcactacctt ctttgactat gcgtcgtatg      780
cgagagtctg tttccaggat gcctgttagt tctcagcaca gatattctac acctcacgcc      840
ttcaccttta acacctccag tccctcatct gaaggttccc tctcccagag gcagagggtc      900
acatccacac ctaatgtcca catggtcagc accacgctgc ctgtggacag caggatgatt      960
gaggatgcaa ttcgaagtca cagcgaatca gcctcacctt cagccctgtc cagtagcccc     1020
aacaatctga gcccaacagg ctggtcacag ccgaaaaccc ccgtgccagc acaaagagag     1080
cgggcaccag tatctgggac ccaggagaaa aacaaaatta ggctcgtgg acagagagat     1140
tcaagctatt attgggaaat agaagccagt gaagtgatgc tgtccactcg gattgggtca     1200
ggctcttttg gaactgttta taagggtaaa tggcacggag atgttgagcgt aaagatccta     1260
aaggttgtcg acccaacccc agagcaattc caggccttca ggaatgaggt ggctgttctg     1320
cgcaaaacac ggcattgtgaa cattctgctt ttcattgggg acatgacaaa ggacaacctg     1380
gcaattgtga ccagtggtg cgagggcagc agcctctaca aacacctgca tgtccaggag     1440
accaagtttc agatgttcca gctaattgac attgcccggc agacggctca gggaatggac     1500
tatttgcatt caaagaacat catccataga gacatgaaa ccaacaatat atttctccat     1560
gaaggcttaa cagtgaataa tggagatttt ggtttggcaa cagtaaagtc acgctggagt     1620
ggttctcagg aggttgaaca acctactggc tctgtcctct ggatggcccc agaggtgatc     1680
cgaatgcagg ataacaaccc attcagtttc cagtcggatg tctactccta tggcatcgta     1740
ttgtatgaac tgatgacggg ggagcttctt tattctcaca tcaacaaccg agatcagatc     1800
atcttcatgg tgggcccagg atatgcctcc ccagatctta gtaagctata taagaactgc     1860
cccaaagcaa tgaagaggct ggtagctgac tgtgtgaaga aagtaaagga agagaggcct     1920
ctttttcccc agatcctgtc ttccattgag ctgctccaac actctctacc gaagatcaac     1980
cggagcgctt ccgagccatc cttgcatcgg gcagcccaca ctgaggatat caatgcttgc     2040

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acgctgacca cgtccccgag gctgcctgtc ttctagttga ctttgcacct gtcttcaggc 2100
tgccagggga ggaggagaag ccagcaggca ccacttttct gctccctttc tccagaggca 2160
gaacacatgt tttcagagaa gctctgctaa ggaccttcta gactgctcac agggccttaa 2220
cttcatgttg ctttcttttc tatccctttg ggccctggga gaaggaagcc atttgcagtg 2280
ctggtgtgtc ctgctccctc cccacattcc ccattgctcaa ggcccagcct tctgtagatg 2340
cgcaagtgga tgttgatggg agtacaaaaa gcagggggccc agccccagct gttgggtaca 2400
tgagtattta gaggaagtaa ggtagcaggc agtccagccc tgatgtggag acacatggga 2460
ttttggaaat cagcttcttg aggaatgcat gtcacaggcg ggactttctt cagagagtgg 2520
tgcagcgcca gacattttgc acataaggca ccaaacagcc caggactgcc gagactctgg 2580
ccgcccgaag gagcctgctt tggactatg gaacttttct taggggacac gtccctcttt 2640
cacagcttct aagggtgtcca gtgcattggg atgggtttcc aggcaaggca ctcgccaat 2700
ccgcatctca gccctctcag gagcagtctt ccattcatgct gaattttgtc ttccaggagc 2760
tgcccttatg gggcgggccg cagggccagc ctgtttctct aacaaacaaa caaacaacaa 2820
gccttgtttc tctagtcaca tcatgtgtat acaaggaagc caggaataca ggttttcttg 2880
atgatttggg ttttaatttt gtttttattg cacctgacaa aatacagtta tctgatggtc 2940
cctcaattat gttatttttaa taaaataaat taaatttt 2977

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&lt;210&gt; 16

&lt;211&gt; 813

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 16

```

Met Ser Arg Ile Asn Phe Lys Lys Ser Ser Ala Ser Thr Thr Pro Thr
 1           5           10           15
Ser Pro His Cys Pro Ser Pro Arg Leu Ile Ser Leu Pro Arg Cys Ala
 20           25           30
Ser Ser Ser Ile Asp Arg Lys Asp Gln Ala Ser Pro Met Ala Ser Pro
 35           40           45
Ser Thr Pro Leu Tyr Pro Lys His Ser Asp Ser Leu His Ser Leu Ser
 50           55           60
Gly His His Ser Ala Gly Gly Ala Gly Thr Ser Asp Lys Glu Pro Pro
 65           70           75           80
Lys Phe Lys Tyr Lys Met Ile Met Val His Leu Pro Phe Asp Gln His
 85           90           95
Ser Arg Val Glu Val Arg Pro Gly Glu Thr Ala Arg Asp Ala Ile Ser
100          105          110
Lys Leu Leu Lys Lys Arg Asn Ile Thr Pro Gln Leu Cys His Val Asn
115          120          125
Ala Ser Ser Asp Pro Lys Gln Glu Ser Ile Glu Leu Ser Leu Thr Met
130          135          140
Glu Glu Ile Ala Ser Arg Leu Pro Gly Asn Glu Leu Trp Val His Ser
145          150          155          160
Glu Tyr Leu Asn Thr Val Ser Ser Ile Lys His Ala Ile Val Arg Arg
165          170          175
Thr Phe Ile Pro Pro Lys Ser Cys Asp Val Cys Asn Asn Pro Ile Trp
180          185          190
Met Met Gly Phe Arg Cys Glu Phe Cys Gln Phe Lys Phe His Gln Arg
195          200          205
Cys Ser Ser Phe Ala Pro Leu Tyr Cys Asp Leu Leu Gln Ser Val Pro
210          215          220
Lys Asn Glu Asp Leu Val Lys Glu Leu Phe Gly Ile Ala Ser Gln Val
225          230          235          240
Glu Gly Pro Asp Arg Ser Val Ala Glu Ile Val Leu Ala Asn Leu Ala
245          250          255
Pro Thr Ser Gly Gln Ser Pro Ala Ala Thr Pro Asp Ser Ser His Pro
260          265          270

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Asp	Leu	Thr	Ser	Ile	Lys	Arg	Thr	Gly	Gly	Val	Lys	Arg	His	Pro	Met	275	280	285
Ala	Val	Ser	Pro	Gln	Asn	Glu	Thr	Ser	Gln	Leu	Ser	Pro	Ser	Gly	Pro	290	295	300
Tyr	Pro	Arg	Asp	Arg	Ser	Ser	Ser	Ala	Pro	Asn	Ile	Asn	Ala	Ile	Asn	305	310	315
Asp	Glu	Ala	Thr	Val	Gln	His	Asn	Gln	Arg	Ile	Leu	Asp	Ala	Leu	Glu	325	330	335
Ala	Gln	Arg	Leu	Glu	Glu	Glu	Ser	Arg	Asp	Lys	Thr	Gly	Ser	Leu	Leu	340	345	350
Ser	Thr	Gln	Ala	Arg	His	Arg	Pro	His	Phe	Gln	Ser	Gly	His	Ile	Leu	355	360	365
Ser	Gly	Ala	Arg	Met	Asn	Arg	Leu	His	Pro	Leu	Val	Asp	Cys	Thr	Pro	370	375	380
Leu	Gly	Ser	Asn	Ser	Pro	Ser	Ser	Thr	Cys	Ser	Ser	Pro	Pro	Gly	Gly	385	390	395
Leu	Ile	Gly	Gln	Pro	Thr	Leu	Gly	Gln	Ser	Pro	Asn	Val	Ser	Gly	Ser	405	410	415
Thr	Thr	Ser	Ser	Leu	Val	Ala	Ala	His	Leu	His	Thr	Leu	Pro	Leu	Thr	420	425	430
Pro	Pro	Gln	Ser	Ala	Pro	Pro	Gln	Lys	Ile	Ser	Pro	Gly	Phe	Phe	Arg	435	440	445
Asn	Arg	Ser	Arg	Ser	Pro	Gly	Glu	Arg	Leu	Asp	Ala	Gln	Arg	Pro	Arg	450	455	460
Pro	Pro	Gln	Lys	Pro	His	His	Glu	Asp	Trp	Glu	Ile	Leu	Pro	Asn	Glu	465	470	475
Phe	Ile	Ile	Gln	Tyr	Lys	Val	Gly	Ser	Gly	Ser	Phe	Gly	Thr	Val	Tyr	485	490	495
Arg	Gly	Glu	Phe	Gly	Thr	Val	Ala	Ile	Lys	Lys	Leu	Asn	Val	Val		500	505	510
Asp	Pro	Thr	Pro	Ser	Gln	Met	Ala	Ala	Phe	Lys	Asn	Glu	Val	Ala	Val	515	520	525
Leu	Lys	Lys	Thr	Arg	His	Leu	Asn	Val	Leu	Leu	Phe	Met	Gly	Trp	Val	530	535	540
Arg	Glu	Pro	Glu	Ile	Ala	Ile	Ile	Thr	Gln	Trp	Cys	Glu	Gly	Ser	Ser	545	550	555
Leu	Tyr	Arg	His	Ile	His	Val	Gln	Glu	Pro	Arg	Val	Glu	Phe	Glu	Met	565	570	575
Gly	Ala	Ile	Ile	Asp	Ile	Leu	Lys	Gln	Val	Ser	Leu	Gly	Met	Asn	Tyr	580	585	590
Leu	His	Ser	Lys	Asn	Ile	Ile	His	Arg	Asp	Leu	Lys	Thr	Asn	Asn	Ile	595	600	605
Phe	Leu	Met	Asp	Asp	Met	Ser	Thr	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	610	615	620
Ala	Thr	Val	Lys	Thr	Lys	Trp	Thr	Val	Asn	Gly	Gln	Gln	Gln	Gln	Gln	625	630	635
Gln	Pro	Thr	Gly	Ser	Ile	Leu	Trp	Met	Ala	Pro	Glu	Val	Ile	Arg	Met	645	650	655
Gln	Asp	Asp	Asn	Pro	Tyr	Thr	Pro	Gln	Ser	Asp	Val	Tyr	Ser	Phe	Gly	660	665	670
Ile	Cys	Met	Tyr	Glu	Ile	Leu	Ser	Ser	His	Leu	Pro	Tyr	Ser	Asn	Ile	675	680	685
Asn	Asn	Arg	Asp	Gln	Ile	Leu	Phe	Met	Val	Gly	Arg	Gly	Tyr	Leu	Arg	690	695	700
Pro	Asp	Arg	Ser	Lys	Ile	Arg	His	Asp	Thr	Pro	Lys	Ser	Met	Leu	Lys	705	710	715
Leu	Tyr	Asp	Asn	Cys	Ile	Met	Phe	Asp	Arg	Asn	Glu	Arg	Pro	Val	Phe	725	730	735
Gly	Glu	Val	Leu	Glu	Arg	Leu	Arg	Asp	Ile	Ile	Leu	Pro	Lys	Leu	Thr	740	745	750

Arg Ser Gln Ser Ala Pro Asn Val Leu His Leu Asp Ser Gln Tyr Ser  
                   755                                  760                                  765  
 Val Met Asp Ala Val Met Arg Ser Gln Met Leu Ser Trp Ser Tyr Ile  
                   770                                  775                                  780  
 Pro Pro Ala Thr Ala Lys Thr Pro Gln Ser Ala Ala Ala Ala Ala Ala  
 785                                  790                                  795                                  800  
 Arg Asn Lys Lys Ala Tyr Tyr Asn Val Tyr Gly Leu Ile  
                                   805                                  810

<210> 17  
 <211> 1044  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
       Synthetic Construct

<400> 17  
 atggagagag acttcgacct tggcatgggc agacctggcg ggctcggagg acttggtggt 60  
 gaaccgatca tgcaacaaat gccacagcca gcgcctcatc atccatcccg tagtagtaac 120  
 gaccacaatg tgaagaacct catgaagcag gccgaggaga actccggata tctcacattg 180  
 caaggttaacc gtcgtaaagc tgacttgaag gagcttcagt tcgtggaaga tattggtcat 240  
 ggaagctgcg gtacgggtcac aaagtgcaga tacaagagtg tgatcatggc tgtgaagacg 300  
 atgcctcggg cgtcaaacag ttatgaaatg tcccgcattt tgatggatct tgacgtcatc 360  
 tgtctctctt tcgactgtcc gtacattgta cgttgcttcg gatacttcat caccaacttc 420  
 gacgtccgtg tctgcatgga gtgcatggct acttgccctg accgtctgct tatccgcac 480  
 aagcagccaa ttccagagag aattattgga aagttgagtg tgagcatcat taaagctctg 540  
 cactacttga aaaccaagca ccaaatcatg caccgtgatg tgaagccatc aaacattctc 600  
 ctcgactgga gtggcgctcat caagctttgc gatttcggta ttgctggcag actgatcgag 660  
 tctcgtgctc attcgaagca agccggatgc cctctgtaca tgggtcctga gcgcctcgac 720  
 cccaacaact ttgactcgta tgacattcgc agtgacgtgt ggtcttttgg tgttactttg 780  
 gtcgagctgg caaccggaca gtaccatac gccggaaccg aattcgacat gatgtccaag 840  
 attctcaatg acgagccacc gcgcctggat ccggccaaat tctctccgga cttctgtcaa 900  
 ctcgtcgaga gctgcctgca gcgtgatcca acgatgcgtc ccaattacga tatgctcctc 960  
 cagcatccgt ttgtcgtgca tcacgagaaa attgaaaccg acgtcgagga gtggtttgcc 1020  
 gatgtgatgg gcgagtgcgg ataa 1044

<210> 18  
 <211> 1493  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/Note =  
       Synthetic Construct

<400> 18  
 Met Ala Ala Ala Ala Gly Asp Arg Ala Ser Ser Ser Gly Phe Pro Gly  
   1                                  5                                  10                                  15  
 Ala Ala Ala Ala Ser Pro Glu Ala Gly Gly Gly Gly Gly Gly Gly Gly  
                   20                                  25                                  30  
 Ala Leu Gln Gly Ser Gly Ala Pro Ala Ala Gly Ala Ala Gly Leu Leu  
                   35                                  40                                  45  
 Arg Glu Pro Gly Ser Ala Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg  
                   50                                  55                                  60  
 Gln Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln  
 65                                  70                                  75                                  80  
 Pro Leu Phe Leu Ala Ala Ala Ser Pro Pro Cys Pro Ser Thr Ser Pro  
                                   85                                  90                                  95

Ser	Pro	Glu	Pro	Ala	Asp	Ala	Ala	Ala	Gly	Ala	Ser	Arg	Phe	Gln	Pro	100	105	110
Ala	Ala	Gly	Pro	Pro	Pro	Pro	Gly	Ala	Ala	Ser	Arg	Cys	Gly	Ser	His	115	120	125
Ser	Ala	Glu	Leu	Ala	Ala	Ala	Arg	Asp	Ser	Gly	Ala	Arg	Ser	Pro	Ala	130	135	140
Gly	Ala	Glu	Pro	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Arg	Glu	Met	Glu	145	150	155
Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	His	Lys	Met	Glu	Asp	Arg	Pro	Glu	165	170	175
Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	Lys	Ala	Thr	Cys	Met	Pro	Ala	Trp	180	185	190
Lys	His	Glu	Trp	Leu	Glu	Arg	Arg	Asn	Arg	Arg	Gly	Pro	Val	Val	Val	195	200	205
Lys	Pro	Ile	Pro	Ile	Lys	Gly	Asp	Gly	Ser	Glu	Val	Asn	Asn	Leu	Ala	210	215	220
Ala	Glu	Pro	Gln	Gly	Glu	Gly	Gln	Ala	Gly	Ser	Ala	Ala	Pro	Ala	Pro	225	230	235
Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	Gly	Ser	Ser	Pro	Ser	Gly	Arg	Ser	245	250	255
Val	Lys	Pro	Glu	Ser	Pro	Gly	Val	Arg	Arg	Lys	Arg	Val	Ser	Pro	Val	260	265	270
Pro	Phe	Gln	Ser	Gly	Arg	Ile	Thr	Pro	Pro	Arg	Arg	Ala	Pro	Ser	Pro	275	280	285
Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	Glu	Glu	Thr	Ser	Arg	Arg	Val	Asn	290	295	300
Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr	Leu	Leu	Gln	Gln	Ile	Gly	Pro	Asn	305	310	315
Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser	Pro	Asp	Asn	Lys	Tyr	Arg	Val	Phe	325	330	335
Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys	Gly	Arg	Gly	Ala	Phe	Cys	Ile	His	340	345	350
Leu	Leu	Phe	Val	Met	Leu	Arg	Val	Phe	Gln	Leu	Glu	Pro	Ser	Asp	Pro	355	360	365
Met	Leu	Trp	Arg	Lys	Thr	Leu	Lys	Asn	Phe	Glu	Val	Glu	Ser	Leu	Phe	370	375	380
Gln	Lys	Tyr	His	Ser	Arg	Arg	Ser	Ser	Arg	Ile	Lys	Ala	Pro	Ser	Arg	385	390	395
Asn	Thr	Ile	Gln	Lys	Phe	Val	Ser	Arg	Met	Ser	Asn	Ser	His	Thr	Leu	405	410	415
Ser	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Glu	Asn	Ser	Ile	Lys	Asp	420	425	430
Glu	Glu	Glu	Gln	Met	Cys	Pro	Ile	Cys	Leu	Leu	Gly	Met	Leu	Asp	Glu	435	440	445
Glu	Ser	Leu	Thr	Val	Cys	Glu	Asp	Gly	Cys	Arg	Asn	Lys	Leu	His	His	450	455	460
His	Cys	Met	Ser	Ile	Trp	Ala	Glu	Glu	Cys	Arg	Arg	Asn	Arg	Glu	Pro	465	470	475
Leu	Ile	Cys	Pro	Leu	Cys	Arg	Ser	Lys	Trp	Arg	Ser	His	Asp	Phe	Tyr	485	490	495
Ser	His	Glu	Leu	Ser	Ser	Pro	Val	Glu	Ser	Pro	Ala	Ser	Leu	Arg	Ala	500	505	510
Val	Gln	Gln	Pro	Ser	Ser	Pro	Gln	Pro	Val	Ala	Gly	Ser	Gln	Arg		515	520	525
Arg	Asn	Gln	Glu	Ser	Ser	Phe	Asn	Leu	Thr	His	Phe	Gly	Thr	Gln	Gln	530	535	540
Ile	Pro	Ser	Ala	Tyr	Lys	Asp	Leu	Ala	Glu	Pro	Trp	Ile	Gln	Val	Phe	545	550	555
Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe	Ser	Arg	Asn	Trp	Asn	Val	Arg	565	570	575

Glu Met Ala Leu Arg Arg Leu Ser His Asp Val Ser Gly Ala Leu Leu	580	585	590
Leu Ala Asn Gly Glu Ser Thr Gly Asn Ser Gly Gly Gly Ser Gly Gly	595	600	605
Ser Leu Ser Ala Gly Ala Ala Ser Gly Ser Ser Gln Pro Ser Ile Ser	610	615	620
Gly Asp Val Val Glu Ala Cys Cys Ser Val Leu Ser Ile Val Cys Ala	625	630	635
Asp Pro Val Tyr Lys Val Tyr Val Ala Ala Leu Lys Thr Leu Arg Ala	645	650	655
Met Leu Val Tyr Thr Pro Cys His Ser Leu Ala Glu Arg Ile Lys Leu	660	665	670
Gln Arg Leu Leu Arg Pro Val Val Asp Thr Ile Leu Val Lys Cys Ala	675	680	685
Asp Ala Asn Ser Arg Thr Ser Gln Leu Ser Ile Ser Thr Val Leu Glu	690	695	700
Leu Cys Lys Gly Gln Ala Gly Glu Leu Ala Val Gly Arg Glu Ile Leu	705	710	715
Lys Ala Gly Ser Ile Gly Val Gly Gly Val Asp Tyr Val Leu Ser Cys	725	730	735
Ile Leu Gly Asn Gln Ala Glu Ser Asn Asn Trp Gln Glu Leu Leu Gly	740	745	750
Arg Leu Cys Leu Ile Asp Arg Leu Leu Leu Glu Phe Pro Ala Glu Phe	755	760	765
Tyr Pro His Ile Val Ser Thr Asp Val Ser Gln Ala Glu Pro Val Glu	770	775	780
Ile Arg Tyr Lys Lys Leu Leu Ser Leu Leu Thr Phe Ala Leu Gln Ser	785	790	795
Ile Asp Asn Ser His Ser Met Val Gly Lys Leu Ser Arg Arg Ile Tyr	805	810	815
Leu Ser Ser Ala Arg Met Val Thr Ala Val Pro Ala Val Phe Ser Lys	820	825	830
Leu Val Thr Met Leu Asn Ala Ser Gly Ser Thr His Phe Thr Arg Met	835	840	845
Arg Arg Arg Leu Met Ala Ile Ala Asp Glu Val Glu Ile Ala Glu Val	850	855	860
Ile Gln Leu Gly Val Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu	865	870	875
Gln Ala Val Ala Pro Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His	885	890	895
Thr Val His Arg Glu Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu	900	905	910
Ser Ala Ser Ser Glu Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val	915	920	925
Gly Leu Pro Ser Ser Thr Thr Glu Gln Pro Lys Pro Ala Val Gln	930	935	940
Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser	945	950	955
His Ala Gln Leu Met Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala	965	970	975
Pro Ser Val Pro Asp Ile Ser Lys His Arg Pro Gln Ala Phe Val Pro	980	985	990
Cys Lys Ile Pro Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu	995	1000	1005
Gln Phe Gln Arg Asn Cys Ser Glu His Arg Asp Ser Asp Gln Leu Ser	1010	1015	1020
Pro Val Phe Thr Gln Ser Arg Pro Pro Pro Ser Ser Asn Ile His Arg	1025	1030	1035
Pro Lys Pro Ser Arg Pro Val Pro Gly Ser Thr Ser Lys Leu Gly Asp	1045	1050	1055

Ala Thr Lys Ser Ser Met Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys  
                   1060                                  1065                                  1070  
 Asp Asp Ser Phe Gly Gly Gly Gly Asn Ser Gly Asn Ala Val Ile Pro  
                   1075                                  1080                                  1085  
 Ser Asp Glu Thr Val Phe Thr Pro Val Glu Asp Lys Cys Arg Leu Asp  
                   1090                                  1095                                  1100  
 Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu Ala Ser  
                   1105                                  1110                                  1115                                  1120  
 Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser Glu Val Ala Val  
                   1125                                  1130                                  1135  
 Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val  
                   1140                                  1145                                  1150  
 Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Glu  
                   1155                                  1160                                  1165  
 Ala Leu Ala Ile Ala Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro  
                   1170                                  1175                                  1180  
 Ile Val Pro Gln Leu Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile  
                   1185                                  1190                                  1195                                  1200  
 Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln  
                   1205                                  1210                                  1215  
 Pro Tyr Arg Glu Asp Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu  
                   1220                                  1225                                  1230  
 Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr  
                   1235                                  1240                                  1245  
 Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu  
                   1250                                  1255                                  1260  
 Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly  
                   1265                                  1270                                  1275                                  1280  
 His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly Ala Thr Cys Glu  
                   1285                                  1290                                  1295  
 Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val  
                   1300                                  1305                                  1310  
 Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile  
                   1315                                  1320                                  1325  
 Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn  
                   1330                                  1335                                  1340  
 Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu Leu Ile Asp Ser  
                   1345                                  1350                                  1355                                  1360  
 Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu  
                   1365                                  1370                                  1375  
 Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly  
                   1380                                  1385                                  1390  
 Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly  
                   1395                                  1400                                  1405  
 Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala  
                   1410                                  1415                                  1420  
 Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His Leu Ala  
                   1425                                  1430                                  1435                                  1440  
 Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser  
                   1445                                  1450                                  1455  
 His Leu Ser Pro Gly Leu Arg Asp Val Ala Val Arg Cys Leu Glu Leu  
                   1460                                  1465                                  1470  
 Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val  
                   1475                                  1480                                  1485  
 Phe Arg Thr Thr Trp  
                   1490

&lt;210&gt; 19

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence



&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 19

```

Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
 1           5           10           15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
      20           25           30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
      35           40           45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
      50           55           60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
65           70           75           80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
      85           90           95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
      100          105          110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
      115          120          125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
      130          135          140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
145          150          155          160
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
      165          170          175
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
      180          185          190
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
      195          200          205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
      210          215          220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
225          230          235          240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
      245          250          255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
      260          265          270
Leu Met Phe Gly Cys Gln Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
      275          280          285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
290          295          300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
305          310          315          320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
      325          330          335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
      340          345          350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
      355          360          365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
      370          375          380
Ser Thr Pro Thr His Ala Ala Gly Val
385          390

```

&lt;210&gt; 20

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 20

```

Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro Asp
 1           5           10           15
Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu Ala
 20           25           30
Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln Arg Lys
 35           40           45
Arg Leu Glu Ala Phe Leu Thr Gln Lys Gln Lys Val Gly Glu Leu Lys
 50           55           60
Asp Asp Asp Phe Glu Lys Ile Ser Glu Leu Gly Ala Gly Asn Gly Gly
 65           70           75           80
Val Val Phe Lys Val Ser His Lys Pro Ser Gly Leu Val Met Ala Arg
 85           90           95
Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg Asn Gln Ile Ile
 100          105          110
Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro Tyr Ile Val Gly
 115          120          125
Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser Ile Cys Met Glu
 130          135          140
His Met Asp Gly Gly Ser Leu Asp Gln Val Leu Lys Lys Ala Gly Arg
 145          150          155          160
Ile Pro Glu Gln Ile Leu Gly Lys Val Ser Ile Ala Val Ile Lys Gly
 165          170          175
Leu Thr Tyr Leu Arg Glu Lys His Lys Ile Met His Arg Asp Val Lys
 180          185          190
Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile Lys Leu Cys Asp
 195          200          205
Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala Asn Ser Phe Val
 210          215          220
Gly Thr Arg Ser Tyr Met Ser Pro Glu Arg Leu Gln Gly Thr His Tyr
 225          230          235          240
Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser Leu Val Glu Met
 245          250          255
Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala Lys Glu Leu Glu
 260          265          270
Leu Leu Phe Gly Cys His Val Glu Gly Asp Ala Ala Glu Thr Pro Pro
 275          280          285
Arg Pro Arg Thr Pro Gly Arg Pro Leu Ser Ser Tyr Gly Met Asp Ser
 290          295          300
Arg Pro Pro Met Ala Ile Phe Glu Leu Leu Asp Tyr Ile Val Asn Glu
 305          310          315          320
Pro Pro Pro Lys Leu Pro Ser Gly Val Phe Ser Leu Glu Phe Gln Asp
 325          330          335
Phe Val Asn Lys Cys Leu Ile Lys Asn Pro Ala Glu Arg Ala Asp Leu
 340          345          350
Lys Gln Leu Met Val His Ala Phe Ile Lys Arg Ser Asp Ala Glu Glu
 355          360          365
Val Asp Phe Ala Gly Trp Leu Cys Ser Thr Ile Gly Leu Asn Gln Pro
 370          375          380
Ser Thr Pro Thr His Ala Ala Ser Ile
 385          390

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&lt;210&gt; 21

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/Note =  
Synthetic Construct

&lt;400&gt; 21

Met	Pro	Lys	Lys	Lys	Pro	Thr	Pro	Ile	Gln	Leu	Asn	Pro	Ala	Pro	Asp
1				5					10					15	
Gly	Ser	Ala	Val	Asn	Gly	Thr	Ser	Ser	Ala	Glu	Thr	Asn	Leu	Glu	Ala
			20					25					30		
Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu	Gln	Gln	Arg	Lys
		35					40					45			
Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Gln	Lys	Val	Gly	Glu	Leu	Lys
	50					55					60				
Asp	Asp	Asp	Phe	Glu	Lys	Ile	Ser	Glu	Leu	Gly	Ala	Gly	Asn	Gly	Gly
65					70					75					80
Val	Val	Phe	Lys	Val	Ser	His	Lys	Pro	Ser	Gly	Leu	Val	Met	Ala	Arg
				85				90						95	
Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Ile	Arg	Asn	Gln	Ile	Ile
			100					105					110		
Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro	Tyr	Ile	Val	Gly
		115					120						125		
Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	Ile	Cys	Met	Glu
	130					135					140				
His	Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	Lys	Ala	Gly	Arg
145					150					155					160
Ile	Pro	Glu	Gln	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala	Val	Ile	Lys	Gly
				165				170						175	
Leu	Thr	Tyr	Leu	Arg	Glu	Lys	His	Lys	Ile	Met	His	Arg	Asp	Val	Lys
			180					185					190		
Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile	Lys	Leu	Cys	Asp
		195				200						205			
Phe	Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	Asn	Ser	Phe	Val
	210					215					220				
Gly	Thr	Arg	Ser	Tyr	Met	Ser	Pro	Glu	Arg	Leu	Gln	Gly	Thr	His	Tyr
225					230					235					240
Ser	Val	Gln	Ser	Asp	Ile	Trp	Ser	Met	Gly	Leu	Ser	Leu	Val	Glu	Met
				245					250					255	
Ala	Val	Gly	Arg	Tyr	Pro	Ile	Pro	Pro	Pro	Asp	Ala	Lys	Glu	Leu	Glu
			260				265						270		
Leu	Met	Phe	Gly	Cys	Gln	Val	Glu	Gly	Asp	Ala	Ala	Glu	Thr	Pro	Pro
		275				280						285			
Arg	Pro	Arg	Thr	Pro	Gly	Arg	Pro	Leu	Ser	Ser	Tyr	Gly	Met	Asp	Ser
	290				295						300				
Arg	Pro	Pro	Met	Ala	Ile	Phe	Glu	Leu	Leu	Asp	Tyr	Ile	Val	Asn	Glu
305					310					315					320
Pro	Pro	Pro	Lys	Leu	Pro	Ser	Gly	Val	Phe	Ser	Leu	Glu	Phe	Gln	Asp
				325					330					335	
Phe	Val	Asn	Lys	Cys	Leu	Ile	Lys	Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu
			340				345						350		
Lys	Gln	Leu	Met	Val	His	Ala	Phe	Ile	Lys	Arg	Ser	Asp	Ala	Glu	Glu
	355					360						365			
Val	Asp	Phe	Ala	Gly	Trp	Leu	Cys	Ser	Thr	Ile	Gly	Leu	Asn	Gln	Pro
	370					375					380				
Ser	Thr	Pro	Thr	His	Ala	Ala	Gly	Val							
385					390										